

1  
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<110> Yu et al.

<120> Neutrokinin-alpha and Neutrokinin-alpha Splice Variants

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<141> 2000-02-22

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<151> 1999-12-03

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&lt;151&gt; 2000-01-14

&lt;160&gt; 38

&lt;170&gt; PatentIn Ver. 2.1

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&lt;211&gt; 1100

&lt;212&gt; DNA

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ccaaccttca aagttcaagt agtcatatgat atg gat gac tcc aca gaa agg gag cag 173  
Met Asp Asp Ser Thr Glu Arg Glu Gln

1 5

tca cgc ctt act tct tgc ctt aag aaa aga gaa gaa atg aaa ctg aag 221  
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Glu Cys Val Ser Ile Leu Pro Arg Lys Glu Ser Pro Ser Val Arg Ser  
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Ser Lys Asp Gly Lys Leu Leu Ala Ala Thr Leu Leu Leu Ala Leu Leu  
45 50 55tct tgc tgc ctc acg gtg tct ttc tac cag gtg gcc gcc ctg caa 365  
Ser Cys Cys Leu Thr Val Val Ser Phe Tyr Gln Val Ala Ala Leu Gln  
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Gly Asp Leu Ala Ser Leu Arg Ala Glu Leu Gln Gly His His Ala Glu  
75 80 85aag ctg cca gca gga gca gga gcc ccc aag gcc ggc atg gag gaa gct 461  
Lys Leu Pro Ala Gly Ala Pro Lys Ala Gly Leu Glu Glu Ala  
90 95 100 105cca gct gtc acc gcg gga ctg aaa atc ttt gaa cca cca gct cca gga 509  
Pro Ala Val Thr Ala Gly Leu Lys Ile Phe Glu Pro Pro Ala Pro Gly  
110 115 120gaa ggc aac tcc agt cag aac agc aga aat aag cgt gcc gtt cag ggt 557  
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125 130 135cca gaa gaa aca gtc act caa gac tgc ttg caa ctg att gca gac agt 605  
Pro Glu Glu Thr Val Thr Gln Asp Cys Leu Gln Leu Ile Ala Asp Ser  
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Glu Thr Pro Thr Ile Gln Lys Gly Ser Tyr Thr Phe Val Pro Trp Leu	
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Leu Ser Phe Lys Arg Gly Ser Ala Leu Glu Glu Lys Glu Asn Lys Ile	
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Leu Val Lys Glu Thr Gly Tyr Phe Ile Tyr Gly Gln Val Leu Tyr	
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act gat aag acc tac gcc atg gga cat cta att cag agg aag aag gtc	797
Thr Asp Lys Thr Tyr Ala Met Gly His Leu Ile Gln Arg Lys Lys Val	
205 210 215	
cat gtc ttt ggg gat gaa ttg agt ctg gtg act ttg ttt cga tgt att	845
His Val Phe Gly Asp Glu Leu Ser Leu Val Thr Leu Phe Arg Cys Ile	
220 225 230	
caa aat atg cct gaa aca <del>ata</del> ccc aat aat tcc tgc tat tca gct ggc	893
Gln Asn Met Pro Glu Thr <del>Leu</del> Pro Asn Asn Ser Cys Tyr Ser Ala Gly	
235 240 245	
att gca aaa ctg gaa gaa gat gaa ctc caa ctt gca ata cca aga	941
Ile Ala Lys Leu Glu Gly Asp Glu Leu Gln Leu Ala Ile Pro Arg	
250 255 260 265	
gaa aat gca caa ata tca ctg gat gaa gat gtc aca ttt ttt ggt gca	989
Glu Asn Ala Gln Ile Ser Leu Asp Gly Asp Val Thr Phe Gly Ala	
270 275 280	
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Arg Lys Glu Ser Pro Ser Val Arg Ser Ser Lys Asp Gly Lys Leu Leu	
35 40 45	
Ala Ala Thr Leu Leu Ala Leu Leu Ser Cys Cys Leu Thr Val Val	
50 55 60	
Ser Phe Tyr Gln Val Ala Ala Leu Gln Gly Asp Leu Ala Ser Leu Arg	
65 70 75 80	

Ala Glu Leu Gln Gly His His Ala Glu Lys Leu Pro Ala Gly Ala Gly  
 85 90 95

Ala Pro Lys Ala Gly Leu Glu Glu Ala Pro Ala Val Thr Ala Gly Leu  
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Lys Ile Phe Glu Pro Pro Ala Pro Gly Glu Gly Asn Ser Ser Gln Asn  
 115 120 125

Ser Arg Asn Lys Arg Ala Val Gln Gly Pro Glu Glu Thr Val Thr Gln  
 130 135 140

Asp Cys Leu Gln Leu Ile Ala Asp Ser Glu Thr Pro Thr Ile Gln Lys  
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Gly Ser Tyr Thr Phe Val Pro Trp Leu Leu Ser Phe Lys Arg Gly Ser  
 165 170 175

Ala Leu Glu Glu Lys Glu Asn Lys Ile Leu Val Lys Glu Thr Gly Tyr  
 180 185 190

Phe Phe Ile Tyr Gly Gln Val Leu Tyr Thr Asp Lys Thr Tyr Ala Met  
 195 200 205

Gly His Leu Ile Gln Arg Lys Lys Val His Val Phe Gly Asp Glu Leu  
 210 215 220

Ser Leu Val Thr Leu Phe Arg Cys Ile Gln Asn Met Pro Glu Thr Leu  
 225 230 235 240

Pro Asn Asn Ser Cys Tyr Ser Ala Gly Ile Ala Lys Leu Glu Glu Gly  
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Asp Glu Leu Gln Leu Ala Ile Pro Arg Glu Asn Ala Gln Ile Ser Leu  
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 35 40 45

Cys Leu Leu His Phe Gly Val Ile Gly Pro Gln Arg Glu Glu Phe Pro  
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Arg Asp Leu Ser Leu Ile Ser Pro Leu Ala Gln Ala Val Arg Ser Ser



Val Val Phe Ser Gly Lys Ala Tyr Ser Pro Lys Ala Thr Ser Ser Pro  
 115 120 125

Leu Tyr Leu Ala His Glu Val Gln Leu Phe Ser Ser Gln Tyr Pro Phe  
 130 135 140

His Val Pro Leu Leu Ser Ser Gln Lys Met Val Tyr Pro Gly Leu Gln  
 145 150 155 160

Glu Pro Trp Leu His Ser Met Tyr His Gly Ala Ala Phe Gln Leu Thr  
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Gln Gly Asp Gln Leu Ser Thr His Thr Asp Gly Ile Pro His Leu Val  
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 35 40 45

Gln Asp Gln Gly Gly Leu Val Thr Glu Thr Ala Asp Pro Gly Ala Gln  
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Ala Gln Gln Gly Leu Gly Phe Gln Lys Leu Pro Glu Glu Glu Pro Glu  
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Thr Asp Leu Ser Pro Gly Leu Pro Ala Ala His Leu Ile Gly Ala Pro  
 85 90 95

Leu Lys Gly Gln Gly Leu Gly Trp Glu Thr Thr Lys Glu Gln Ala Phe  
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Leu Thr Ser Gly Thr Gln Phe Ser Asp Ala Glu Gly Leu Ala Leu Pro  
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Ala Pro Pro Gly Gly Asp Pro Gln Gly Arg Ser Val Thr Leu Arg  
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Ser Ser Leu Tyr Arg Ala Gly Gly Ala Tyr Gly Pro Gly Thr Pro Glu  
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Leu Leu Leu Glu Gly Ala Glu Thr Val Thr Pro Val Leu Asp Pro Ala  
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Arg Arg Gln Gly Tyr Gly Pro Leu Trp Tyr Thr Ser Val Gly Phe Gly  
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 35 40 45

Pro Pro Pro Pro Pro Leu Pro Pro Pro Pro Pro Pro Pro Leu Pro  
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Pro Leu Pro Leu Pro Pro Leu Lys Lys Arg Gly Asn His Ser Thr Gly  
 65 70 75 80

Leu Cys Leu Leu Val Met Phe Phe Met Val Leu Val Ala Leu Val Gly  
 85 90 95

Leu Gly Leu Gly Met Phe Gln Leu Phe His Leu Gln Lys Glu Leu Ala  
 100 105 110

Glu Leu Arg Glu Ser Thr Ser Gln Met His Thr Ala Ser Ser Leu Glu  
 115 120 125

Lys Gln Ile Gly His Pro Ser Pro Pro Glu Lys Lys Glu Leu Arg  
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Lys Val Ala His Leu Thr Gly Lys Ser Asn Ser Arg Ser Met Pro Leu  
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Glu Trp Glu Asp Thr Tyr Gly Ile Val Leu Leu Ser Gly Val Lys Tyr  
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Lys Lys Gly Gly Leu Val Ile Asn Glu Thr Gly Leu Tyr Phe Val Tyr  
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Ser Lys Val Tyr Phe Arg Gly Gln Ser Cys Asn Asn Leu Pro Leu Ser  
 195 200 205

His Lys Val Tyr Met Arg Asn Ser Lys Tyr Pro Gln Asp Leu Val Met  
 210 215 220

Met Glu Gly Lys Met Met Ser Tyr Cys Thr Thr Gly Gln Met Trp Ala  
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Arg Ser Ser Tyr Leu Gly Ala Val Phe Asn Leu Thr Ser Ala Asp His  
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agtctggta ctttgggttcg atgtattcaa aatatgcctg aaacactacc caataattcc 180
tgctattcag ctggcattgc aaaaactggna ggaaggagat gaactccaaac ttgcaataacc 240
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aactgctgtg acctncttac antangtgcgt gttncttatt ttnctnctt nttctntgg 360
aacctcttag gaaggaaggaa ttcttaatgc gggaaataacc caaaaaaaann taaaanggg 420
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 aaacaccaac tataaaaaa ggctcccttc tgntgccaca tttgggccaa ggaatggaga 240  
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 caaaggaaaa tctctactta gattnacaca tttgttccca tgggtntctt aagttttaaa 360  
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26

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aag aaa aga gaa gaa atg aaa ctg aag gag tgt gtt tcc atc ctc cca 96  
 Lys Lys Arg Glu Glu Met Lys Leu Lys Glu Cys Val Ser Ile Leu Pro  
 20 25 30

cgg aag gaa agc ccc tct gtc cga tcc tcc aaa gac gga aag ctg ctg 144  
 Arg Lys Glu Ser Pro Ser Val Arg Ser Ser Lys Asp Gly Lys Leu Leu  
 35 40 45

gct gca acc ttg ctg ctg gca ctg ctg tct tgc tgc ctc acg gtg gtg 192  
 Ala Ala Thr Leu Leu Ala Leu Leu Ser Cys Cys Leu Thr Val Val  
 50 55 60

tct ttc tac cag gtg gcc ctg caa ggg gac ctg gcc agc ctc cgg 240  
 Ser Phe Tyr Gln Val Ala Ala Leu Gln Gly Asp Leu Ala Ser Leu Arg  
 65 70 75 80

gca gag ctg cag ggc cac cac gcg gag aag ctg cca gca gga gca gga 288  
 Ala Glu Leu Gln Gly His His Ala Glu Lys Leu Pro Ala Gly Ala Gly

16	85	90	95	
gcc ccc aag gcc ggc ctg gag gaa gct cca gct gtc acc gcg gga ctg Ala Pro Lys Ala Gly Leu Glu Ala Pro Ala Val Thr Ala Gly Leu 100 105 110				336
aaa atc ttt gaa cca cca gct cca gga gaa ggc aac tcc agt cag aac Lys Ile Phe Glu Pro Pro Ala Pro Gly Glu Gly Asn Ser Ser Gln Asn 115 120 125				384
agc aga aat aag cgt gcc gtt cag ggt cca gaa gaa aca gga tct tac Ser Arg Asn Lys Arg Ala Val Gln Gly Pro Glu Glu Thr Gly Ser Tyr 130 135 140				432
aca ttt gtt cca tgg ctt ctc agc ttt aaa agg gga agt gcc cta gaa Thr Phe Val Pro Trp Leu Leu Ser Phe Lys Arg Gly Ser Ala Leu Glu 145 150 155 160				480
gaa aaa gag aat aaa ata ttg gtc aaa gaa act ggt tac ttt ttt ata Glu Lys Glu Asn Lys Ile Leu Val Lys Glu Thr Gly Tyr Phe Phe Ile 165 170 175				528
tat ggt cag gtt tta tat act gat aag acc tac gcc atg gga cat cta Tyr Gly Gln Val Leu Tyr Thr Asp Lys Thr Tyr Ala Met Gly His Leu 180 185 190				576
att cag agg aag aag gtc cat gtc ttt ggg gat gaa ttg agt ctg gtg Ile Gln Arg Lys Lys Val His Val Phe Gly Asp Glu Leu Ser Leu Val 195 200 205				624
act ttg ttt cga tgt att caa aat atg cct gaa aca cta ccc aat aat Thr Leu Phe Arg Cys Ile Gln Asn Met Pro Glu Thr Leu Pro Asn Asn 210 215 220				672
tcc tgc tat tca gct ggc att gca aaa ctg gaa gaa gga gat gaa ctc Ser Cys Tyr Ser Ala Gly Ile Ala Lys Leu Glu Glu Gly Asp Glu Leu 225 230 235 240				720
caa ctt gca ata cca aga gaa aat gca caa ata tca ctg gat gga gat Gln Leu Ala Ile Pro Arg Glu Asn Ala Gln Ile Ser Leu Asp Gly Asp 245 250 255				768
gtc aca ttt ttt ggt gca ttg aaa ctg ctg tgacccactt acaccatgtc Val Thr Phe Phe Gly Ala Leu Lys Leu Leu	260	265		818
tgttagctatt ttccctccctt tctctgtacc tctaagaaga aagaatctaa ctgaaaatac				878
aaaaaaaaaaaa aaaaaaaaaa aaaaaa				903
<pre> &lt;210&gt; 19 &lt;211&gt; 266 &lt;212&gt; PRT &lt;213&gt; Homo sapiens </pre>				
<pre> &lt;400&gt; 19 Met Asp Asp Ser Thr Glu Arg Glu Gln Ser Arg Leu Thr Ser Cys Leu 1 5 10 15 </pre>				

Lys Lys Arg Glu Glu Met Lys Leu Lys Glu Cys Val Ser Ile Leu Pro  
 20 25 30

Arg Lys Glu Ser Pro Ser Val Arg Ser Ser Lys Asp Gly Lys Leu Leu  
 35 40 45

Ala Ala Thr Leu Leu Leu Ala Leu Leu Ser Cys Cys Leu Thr Val Val  
 50 55 60

Ser Phe Tyr Gln Val Ala Ala Leu Gln Gly Asp Leu Ala Ser Leu Arg  
 65 70 75 80

Ala Glu Leu Gln Gly His His Ala Glu Lys Leu Pro Ala Gly Ala Gly  
 85 90 95

Ala Pro Lys Ala Gly Leu Glu Glu Ala Pro Ala Val Thr Ala Gly Leu  
 100 105 110

Lys Ile Phe Glu Pro Pro Ala Pro Gly Glu Gly Asn Ser Ser Gln Asn  
 115 120 125

Ser Arg Asn Lys Arg Ala Val Gln Gly Pro Glu Glu Thr Gly Ser Tyr  
 130 135 140

Thr Phe Val Pro Trp Leu Leu Ser Phe Lys Arg Gly Ser Ala Leu Glu  
 145 150 155 160

Glu Lys Glu Asn Lys Ile Leu Val Lys Glu Thr Gly Tyr Phe Phe Ile  
 165 170 175

Tyr Gly Gln Val Leu Tyr Thr Asp Lys Thr Tyr Ala Met Gly His Leu  
 180 185 190

Ile Gln Arg Lys Lys Val His Val Phe Gly Asp Glu Leu Ser Leu Val  
 195 200 205

Thr Leu Phe Arg Cys Ile Gln Asn Met Pro Glu Thr Leu Pro Asn Asn  
 210 215 220

Ser Cys Tyr Ser Ala Gly Ile Ala Lys Leu Glu Glu Gly Asp Glu Leu  
 225 230 235 240

Gln Leu Ala Ile Pro Arg Glu Asn Ala Gln Ile Ser Leu Asp Gly Asp  
 245 250 255

Val Thr Phe Phe Gly Ala Leu Lys Leu Leu  
 260 265

<210> 20  
 <211> 136  
 <212> PRT  
 <213> Homo sapiens

<400> 20  
 His Ser Val Leu His Leu Val Pro Ile Asn Ala Thr Ser Lys Asp Asp  
 1 5 10 15

Ser Asp Val Thr Glu Val Met Trp Gln Pro Ala Leu Arg Arg Gly Arg

18

20

25

30

Gly Leu Gln Ala Gln Gly Tyr Gly Val Arg Ile Gln Asp Ala Gly Val  
35 40 45

Tyr Leu Leu Tyr Ser Gln Val Leu Phe Gln Asp Val Thr Phe Thr Met  
50 55 60

Gly Gln Val Val Ser Arg Glu Gly Gln Gly Arg Gln Glu Thr Leu Phe  
65 70 75 80

Arg Cys Ile Arg Ser Met Pro Ser His Pro Asp Arg Ala Tyr Asn Ser  
85 90 95

Cys Tyr Ser Ala Gly Val Phe His Leu His Gln Gly Asp Ile Leu Ser  
100 105 110

Val Ile Ile Pro Arg Ala Arg Ala Lys Leu Asn Leu Ser Pro His Gly  
115 120 125

Thr Phe Leu Gly Phe Val Lys Leu  
130 135

<210> 21  
<211> 462  
<212> DNA  
<213> Homo sapiens

<400> 21  
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tctgaaactc cgaccatcca gaaaggttt tacacctttg ttccttggct gctttcttc 120  
aaacgtggtt ctgcccgtga agagaaaagaa aacaaaatcc tggtaaaga aactggttac 180  
ttcttatct acggtcagtt tcttacact gataagacct acggcatggg tcacctgatt 240  
cagcgtaaga aagttcacgt ttcggtgac gagctgtctc tggtaactct gtttcgtgc 300  
attcagaaca tgccggaaac tcttcttaac aactctgtct actctgtgg catcgaaaa 360  
ctggaaagagg gtgatgaact gcagctggca attctctgtg aaaacgcaca aatttctctg 420  
gacggtgatg taacccttctt tggtgactg aaacttctgt aa 462

<210> 22  
<211> 1040  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (1)..(468)

<400> 22  
cgc gtg gta gac ctc tca gct cct gca cca tgc ctg cct gga tgc 48  
Arg Val Val Asp Leu Ser Ala Pro Pro Ala Pro Cys Leu Pro Gly Cys  
1 5 10 15

cgc cat tct caa cat gat gat aat gga atg aac ctc aga aac aga act 96  
Arg His Ser Gln His Asp Asp Asn Gly Met Asn Leu Arg Asn Arg Thr  
20 25 30

tac aca ttt gtt cca tgg ctt ctc agc ttt aaa aga gga aat gcc ttg  
Tyr Thr Phe Val Pro Trp Leu Leu Ser Phe Lys Arg Gly Asn Ala Leu  
144

35

40

45

gag gag aaa gag aac aaa ata gtg gtg agg caa aca ggc tat ttc ttc	192
Glu Glu Lys Glu Asn Lys Ile Val Val Arg Gln Thr Gly Tyr Phe Phe	
50 55 60	
atc tac agc cag gtt cta tac acg gac ccc atc ttt gct atg ggt cat	240
Ile Tyr Ser Gln Val Leu Tyr Thr Asp Pro Ile Phe Ala Met Gly His	
65 70 75 80	
gtc atc dag agg aag aaa gta cac gtc ttt ggg gac gag ctg agc ctg	288
Val Ile Gln Arg Lys Lys Val His Val Phe Gly Asp Glu Leu Ser Leu	
85 90 95	
gtg acc ctg ttc cga tgt att cag aat atg ccc aaa aca ctg ccc aac	336
Val Thr Leu Phe Arg Cys Ile Gln Asn Met Pro Lys Thr Leu Pro Asn	
100 105 110	
aat tcc tgc tac tcg gct ggc atc gcg agg ctg gaa gaa gga gat gag	384
Asn Ser Cys Tyr Ser Ala Gly Ile Ala Arg Leu Glu Glu Gly Asp Glu	
115 120 125	
att cag ctt gca att oct cgg gag aat gca cag att tca cgc aac gga	432
Ile Gln Leu Ala Ile Pro Arg Glu Asn Ala Gln Ile Ser Arg Asn Gly	
130 135 140	
gac gac acc ttc ttt ggt gcc <sup>B</sup> aaa ctg ctg taa ctcacttgct	478
Asp Asp Thr Phe Phe Gly Ala Leu Lys Leu Leu	
145 150 155	
ggagtgcgtg atccccttcc ctcgtcttct ctgtacctcc gagggagaaa cagacgactg	538
gaaaaactaa aagatgggaa aagccgtcag cgaaagttt ctcgtgaccc gttgaatctg	598
atccaaacca ggaaatataa cagacagccca caaccgaagt gtgccatgtg agttatgaga	658
aacggagccc gcgctcagaa agaccggatg aggaagaccg ttttctccag tccttgcca	718
acacgcaccc caacccttgct tttgccttg ggtgacacat gttcagaatg cagggagatt	778
tccttgcattt gcgatttgcc atgagaagag ggcccacaac tgcaggtcac tgaagcattc	838
acgctaagtc tcaggattta ctctcccttc tcatgctaag tacacacacg ctctttcca	898
ggtaatacta tggataacta tggaaagggtt gtttgcattt aaatctagaa gtcttgaact	958
ggcaatagac aaaaatcctt ataaattcaa gtgtaaaata aacttaatta aaaaggttta	1018
agtgtgaaaa aaaaaaaaaa aa	1040

&lt;210&gt; 23

&lt;211&gt; 155

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 23

Arg Val Val Asp Leu Ser Ala Pro Pro Ala Pro Cys Leu Pro Gly Cys

1	5	20	10	15											
Arg	His	Ser	Gln	His	Asp	Asp	Asn	Gly	Met	Asn	Leu	Arg	Asn	Arg	Thr
					20				25						30
Tyr	Thr	Phe	Val	Pro	Trp	Leu	Leu	Ser	Phe	Lys	Arg	Gly	Asn	Ala	Leu
					35				40						45
Glu	Glu	Lys	Glu	Asn	Lys	Ile	Val	Val	Arg	Gln	Thr	Gly	Tyr	Phe	Phe
					50				55						60
Ile	Tyr	Ser	Gln	Val	Leu	Tyr	Thr	Asp	Pro	Ile	Phe	Ala	Met	Gly	His
					65				70						80
Val	Ile	Gln	Arg	Lys	Lys	Val	His	Val	Phe	Gly	Asp	Glu	Leu	Ser	Leu
					85				90						95
Val	Thr	Leu	Phe	Arg	Cys	Ile	Gln	Asn	Met	Pro	Lys	Thr	Leu	Pro	Asn
					100				105						110
Asn	Ser	Cys	Tyr	Ser	Ala	Gly	Ile	Ala	Arg	Leu	Glu	Glu	Gly	Asp	Glu
					115				120						125
Ile	Gln	Leu	Ala	Ile	Pro	Arg	Glu	Asn	Ala	Gln	Ile	Ser	Arg	Asn	Gly
					130				135						140
Asp	Asp	Thr	Phe	Phe	Gly	Ala	Leu	Lys	Leu	Leu					
					145				150						155

<210> 24  
<211> 26  
<212> DNA  
<213> Homo sapiens

<400> 24  
ccaccagctc caggagaagg caactc 

26

<210> 25  
<211> 19  
<212> DNA  
<213> Homo sapiens

<400> 25  
accgcgggac tgaaaatct

19

<210> 26  
<211> 23  
<212> DNA  
<213> Homo sapiens

<400> 26  
cacgcttatt tctgctgttc tga

23

<210> 27  
<211> 657  
<212> DNA  
<213> Homo sapiens

<400> 27  
taccaggatgg cggccgtgca aggggacctg gccagcctcc gggcagagct gcagggccac 60  
cacgcggaga agctgccagc aagagcaaga gcccccaagg ccggctctggg ggaagctcca 120  
gctgtcaccg caggactgaa aatctttgaa ccaccagctc caggagaagg taactccagt 180  
cagagcagca gaaataagcg tgctattcag ggtgcagaag aaacagtcat tcaagactgc 240  
ttgcaactga ttgcagacag tgaacacacca actatacaca aaggatctta cacattgtt 300

ccatggcttc tcagctttaa aaggggaaat gcccctagaag aaaaagagaa taaaatattg 360  
 gtcaaagaaa ctggttactt ttttatataat ggtcagggtt tataactga taagacctat 420  
 gccatggac atctaattca gaggaaaaaa gtccatgtct ttggggatga attgagtcgt 480  
 gtgactttgt ttcgatgtat tcaaaaatatg cctgaaacac tacccataaa ttccctgtat 540  
 ttggctggca ttgcaaaact ggaagaagga gatgaacttc aacttgcata accacqagaa 600  
 aatgcacaaa tatcaactgga tggagatgtc acatttttg gtgccctcaa actgctg 657

<210> 28

<211> 219

<212> PRT

<213> Homo sapiens

<400> 28

Tyr Gln Val Ala Ala Val Gln Gly Asp Leu Ala Ser Leu Arg Ala Glu  
 1 5 10 15

Leu Gln Gly His His Ala Glu Lys Leu Pro Ala Arg Ala Arg Ala Pro  
 20 25 30

Lys Ala Gly Leu Gly Glu Ala Pro Ala Val Thr Ala Gly Leu Lys Ile  
 35 40 45

Phe Glu Pro Pro Ala Pro Gly Glu Gly Asn Ser Ser Gln Ser Ser Arg  
 50 55 60

Asn Lys Arg Ala Ile Gln Gly Ala Glu Glu Thr Val Ile Gln Asp Cys  
 65 70 75 80

Leu Gln Leu Ile Ala Asp Ser Glu Thr Pro Thr Ile Gln Lys Gly Ser  
 85 90 95

Tyr Thr Phe Val Pro Trp Leu Leu Ser Phe Lys Arg Gly Ser Ala Leu  
 100 105 110

Glu Glu Lys Glu Asn Lys Ile Leu Val Lys Glu Thr Gly Tyr Phe Phe  
 115 120 125

Ile Tyr Gly Gln Val Leu Tyr Thr Asp Lys Thr Tyr Ala Met Gly His  
 130 135 140

Leu Ile Gln Arg Lys Lys Val His Val Phe Gly Asp Glu Leu Ser Leu  
 145 150 155 160

Val Thr Leu Phe Arg Cys Ile Gln Asn Met Pro Glu Thr Leu Pro Asn  
 165 170 175

Asn Ser Cys Tyr Ser Ala Gly Ile Ala Lys Leu Glu Glu Gly Asp Glu  
 180 185 190

Leu Gln Leu Ala Ile Pro Arg Glu Asn Ala Gln Ile Ser Leu Asp Gly  
 195 200 205

Asp Val Thr Phe Phe Gly Ala Leu Lys Leu Leu  
 210 215

<210> 29

<211> 657

<212> DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 29

taccagggtgg cggccgtgca aggggacctg gccagcctcc gggcagagct gcagagccac 60  
 catgcggaga agctgccagc aagagcaaga gcccccaagg ccggctctggg ggaagctcca 120  
 gcttcaccg cgggactgaa aatcttgc aaaccagctc caggagaagg caactccagt 180  
 cagacccagca gaaataagcg tgctattcag ggtcagaagg aaacagtcat tcaagactgc 240  
 ttgcactga ttgcagacag tgaaacacca actatacaa aaggatctt cacattgtt 300  
 ccatggttc tcagcttta aaggggaaat gcccataag aaaaagagaa taaaatattg 360  
 gtcaaaagaaa ctggttactt ttttatata ggtcagggtt tataactga taagacctat 420  
 gccatggac atctaattca gagaaaaaa gtccatgtct ttggggatga attgagtcg 480  
 gtgactttgt ttcgatgtat tcaaaatatg cctgaaacac tacccaataa ttcctgctat 540  
 tcagctggca ttgcacaaact ggaagaaggg gatgaacttc aacttgcac accacgagaa 600  
 aatgcacaaa tatactgga tggagatgtc acatttttgc gtgcctcaa actgctg 657

&lt;210&gt; 30

&lt;211&gt; 219

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 30

Tyr	Gln	Val	Ala	Ala	Val	Gln	Gly	Asp	Leu	Ala	Ser	Leu	Arg	Ala	Glu
1					5					10				15	

Leu	Gln	Ser	His	His	Ala	Glu	Lys	Leu	Pro	Ala	Arg	Ala	Arg	Ala	Pro
								20		25			30		

Lys	Ala	Gly	Leu	Gly	Glu	Ala	Pro	Ala	Val	Thr	Ala	Gly	Leu	Lys	Ile
								35	40				45		

Phe	Glu	Pro	Pro	Ala	Pro	Gly	Glu	Gly	Asn	Ser	Ser	Gln	Ser	Ser	Arg
						50	55				60				

Asn	Lys	Arg	Ala	Ile	Gln	Gly	Ala	Glu	Glu	Thr	Val	Ile	Gln	Asp	Cys
					65			70		75			80		

Leu	Gln	Leu	Ile	Ala	Asp	Ser	Glu	Thr	Pro	Thr	Ile	Gln	Lys	Gly	Ser
					85				90			95			

Tyr	Thr	Phe	Val	Pro	Trp	Leu	Leu	Ser	Phe	Lys	Arg	Gly	Ser	Ala	Leu
					100				105				110		

Glu	Glu	Lys	Glu	Asn	Lys	Ile	Leu	Val	Lys	Glu	Thr	Gly	Tyr	Phe	Phe
						115		120			125				

Ile	Tyr	Gly	Gln	Val	Leu	Tyr	Thr	Asp	Lys	Thr	Tyr	Ala	Met	Gly	His
					130		135			140					

Leu	Ile	Gln	Arg	Lys	Lys	Val	His	Val	Phe	Gly	Asp	Glu	Leu	Ser	Leu
						145		150		155			160		

Val	Thr	Leu	Phe	Arg	Cys	Ile	Gln	Asn	Met	Pro	Glu	Thr	Leu	Pro	Asn
						165			170			175			

Asn	Ser	Cys	Tyr	Ser	Ala	Gly	Ile	Ala	Lys	Leu	Glu	Gly	Asp	Glu	
						180		185			190				

Leu	Gln	Leu	Ala	Ile	Pro	Arg	Glu	Asn	Ala	Gln	Ile	Ser	Leu	Asp	Gly
					195			200			205				

Asp Val Thr Phe Phe Gly Ala Leu Lys Leu Leu  
 210 215

<210> 31  
 <211> 38  
 <212> DNA  
 <213> Homo sapiens

<400> 31  
 ggtcgccgtt tctaacgcgg ccgttcaggg tccagaag

38

<210> 32  
 <211> 49  
 <212> DNA  
 <213> Homo sapiens

<400> 32  
 ctggttcggc ccaaggtacc aagcttgtac cttagatctt ttctagatc

49

<210> 33  
 <211> 21  
 <212> DNA  
 <213> Homo sapiens

<400> 33  
 ctggtagttc ttccggagtgt g

21

<210> 34  
 <211> 19  
 <212> DNA  
 <213> Homo sapiens

<400> 34  
 cgcgttagaa acggcgacc

19

<210> 35  
 <211> 22  
 <212> DNA  
 <213> Homo sapiens

<220>  
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 <222> (7)  
 <223> n equals deoxyinosine

<220>  
 <221> misc\_feature  
 <222> (12)  
 <223> n equals deoxyinosine

<220>  
 <221> misc\_feature  
 <222> (16)  
 <223> n equals deoxyinosine

<400> 35  
taccagntgg cngccntgca ag

22

<210> 36  
<211> 22  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (3)  
<223> n equals deoxyinosine

<220>  
<221> misc\_feature  
<222> (14)  
<223> n equals deoxyinosine

<220>  
<221> misc\_feature  
<222> (16)..(17)  
<223> n equals deoxyinosine

<400> 36  
gttnacagcag tttnanngca cc

22

<210> 37  
<211> 866  
<212> DNA  
<213> Mus musculus

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gaagatatga aagtggata tgatcccattc actccgcaga aggaggaggg tgcctggttt 120  
gggatctgca gggatgaaag gctgctggct gctaccctcc tgctggccct gttgtccagc 180  
agtttcacag cgatgtccctt gtaccaggttt gatgccttgc aagcagacct gatgaacctg 240  
cgcatggagc tgcagagctt cccgagggttca gcaacaccagg ccgcgcggg tgctccagag 300  
ttgaccgctg gagtccaaact cctgacacccg gcatgtccctc gaccaccacaa ctccagccgc 360  
ggccacacca acagacgcgc cttccaggga ccagaggaaa cagaacaaga tgttagaccc 420  
tcagtcctc ctgcaccatc cctggcttggc tgccgcatt ctcaacatga tgataatgg 480  
atgaacctca gaaacatcat tcaagactgt ctgcagcttgc ttgagacagcg cgacacgcgg 540  
gccttggagg agaaaagagaa caaaatagtg gtgaggcaaa caggctattt cttcatctac 600  
agccagggttcc tatacacggc ccccatctt gctatgggtc atgtcatccca gaggaagaaa 660  
gtacacgttc ttggggacga gctgagctg gtgaccctgt tccgatgtat tcagaatatg 720  
ccccaaaacac tgcccaacaa ttcttgctac tcggctggca tcggcaggct ggaagaagga 780  
gatgagattc agcttgcaat tcctcgggag aatgcacacaga ttccacgca cggagacgac 840  
accttctttt gtgccttaaa actgt 866

<210> 38  
<211> 177  
<212> PRT  
<213> Mus musculus

<400> 38  
Met Asp Ser Ala Lys Thr Cys Cys Cys Ser Lys Gly Asp Met Lys Val  
1 5 10 15

25

Gly Tyr Asp Thr Lys Gly Ala Trp Gly Cys Arg Asp Gly Arg Ala Ala  
20 25 30

Thr Ala Ser Ser Ser Thr Ala Met Ser Tyr Ala Ala Ala Asp Met Asn  
35 40 45

Arg Met Ser Tyr Arg Gly Ser Ala Thr Ala Ala Ala Gly Ala Thr Ala  
50 55 60

Gly Val Lys Thr Ala Ala Arg His Asn Ser Ser Arg Gly His Arg Asn  
65 70 75 80

Arg Arg Ala Gly Thr Asp Val Asp Ser Ala Ala Cys Gly Cys Arg His  
85 90 95

Ser His Asp Asp Asn Gly ~~Met~~ Asn Arg Asn Asp Cys Ala Asp Ser Asp  
100 105 110

Thr Ala Lys Asn Lys Val Val Arg Thr Gly Tyr Tyr Ser Val Tyr Thr  
115 120 125

Asp Ala Met Gly His Val Arg Lys Lys Val His Val Gly Asp Ser Val  
130 135 140

Thr Arg Cys Asn Met Lys Thr Asn Asn Ser Cys Tyr Ser Ala Gly Ala  
145 150 155 160

Arg Gly Asp Ala Arg Asn Ala Ser Arg Asn Gly Asp Asp Thr Gly Ala  
165 170 175

Lys